

(FILE 'HOME' ENTERED AT 09:15:59 ON 14 JAN 2005)

FILE 'STNGUIDE' ENTERED AT 09:16:12 ON 14 JAN 2005

FILE 'HOME' ENTERED AT 09:16:20 ON 14 JAN 2005

FILE 'CPLUS' ENTERED AT 09:16:44 ON 14 JAN 2005

L1 0 S RSKS

FILE 'MEDLINE, USPATFULL, CPLUS' ENTERED AT 09:17:33 ON 14 JAN 2005

L2 4 S (RSKS)

L3 4 DUP REM L2 (0 DUPLICATES REMOVED)

L3 ANSWER 1 OF 4 USPATFULL on STN
TI Platelet-derived growth factor D
IN Eriksson, Ulf, Stockholm, SWEDEN
Aase, Karin, Stockholm, SWEDEN
Lee, Xuri, Stockholm, SWEDEN
Ponten, Annica, Stockholm, SWEDEN
Uutela, Marko, Helsinki, FINLAND
Alitalo, Kari, Helsinki, FINLAND
Oestman, Arne, Uppsala, SWEDEN
Heldin, Carl-Henrik, Uppsala, SWEDEN

L3 ANSWER 2 OF 4 USPATFULL on STN
TI Method for stimulating connective tissue growth or wound healing
IN Uutela, Marko, University of Helsinki, FINLAND
Eriksson, Ulf, Stockholm, SWEDEN
Alitalo, Kari, University of Helsinki, FINLAND

L3 ANSWER 3 OF 4 USPATFULL on STN
TI Platelet-derived growth factor D, DNA coding therefor, and uses thereof
IN Eriksson, Ulf, Stockholm, SWEDEN
Aase, Karin, Stockholm, SWEDEN
Li, Xuri, Stockholm, SWEDEN
Ponten, Annica, Stockholm, SWEDEN
Uutela, Marko, Helsinki, FINLAND
Alitalo, Kari, Helsinki, FINLAND
Oestman, Arne, Uppsala, SWEDEN
Heldin, Carl-Henrik, Uppsala, SWEDEN

L3 ANSWER 4 OF 4 USPATFULL on STN
TI Process and apparatus for testing the uniformity of pneumatic tires
IN Himmller, Gunther, Darmstadt, Germany, Federal Republic of

L3 ANSWER 1 OF 4 USPATFULL on STN

SUMM . . . of PDGF-D. The portion of the PVHD is from residues 254-370 of FIG. 8 where the putative proteolytic processing site **RKSK** starts at amino acid residue 254 (SEQ ID NO:8). However, the PVHD extends toward the N terminus up to residue. . .

SUMM . . . an active PDGF/VEGF homology domain. A putative proteolytic site is found in residues 255-258 in the full length protein, residues - **RKSK-** (SEQ ID NO:9). This is a dibasic motif. The -**RKSK** - (SEQ ID NO:9) putative proteolytic site is also found in PDGF-A, PDGF-B, VEGF-C and VEGF-D. In these four proteins, the putative. . .

CLM What is claimed is:

. . . any one of claim 1, claim 8 or claim 5 which comprises a proteolytic site having the amino acid sequence **RKSK** (SEQ ID NO: 9).

L3 ANSWER 2 OF 4 USPATFULL on STN

SUMM . . . portion of the PVHD is from residues 254-370 of FIG. 8 (SEQ ID NO:8) where the putative proteolytic processing site **RKSK** starts at amino acid residue 254 (SEQ ID NO:8). However, the PVHD extends toward the N terminus up to residue. . .

SUMM . . . an active PDGF/VEGF homology domain. A putative proteolytic site is found in residues 254-257 in the full length protein, residues - **RKSK-** (SEQ ID NO:9). This is a dibasic motif. The -**RKSK** - (SEQ ID NO:9) putative proteolytic site is also found in PDGF-A, PDGF-B, VEGF-C and VEGF-D. In these four proteins, the. . .

SUMM . . . having the biological activity of PDGF-D and a polypeptide thereof which comprises a proteolytic site having the amino acid sequence **RKSK** (SEQ ID NO:9) or a structurally conserved amino acid sequence thereof.

L3 ANSWER 3 OF 4 USPATFULL on STN

SUMM . . . portion of the PVHD is from residues 255-371 of FIG. 8 (SEQ ID NO:8) where the putative proteolytic processing site **RKSK** starts at amino acid residue 255 (SEQ ID NO:8). However, the PVHD extends toward the N terminus up to residue. . .

SUMM . . . an active PDGF/VEGF homology domain. A putative proteolytic site is found in residues 255-258 in the full length protein, residues - **RKSK-** (SEQ ID NO:9). This is a dibasic motif. The -**RKSK** - (SEQ ID NO:9) putative proteolytic site is also found in PDGF-A, PDGF-B, VEGF-C and VEGF-D. In these four proteins, the putative. . .

CLM What is claimed is:

. . . isolated nucleic acid molecule according to claim 1, wherein the polypeptide comprises a proteolytic site having the amino acid sequence **RKSK** or a structurally conserved amino acid sequence thereof.

L3 ANSWER 4 OF 4 USPATFULL on STN

DETD . . . by radial or rotational truth defects of the testing drum 1. That corrected radial force fluctuation signal is identified by **RKSk** (ψ).

DETD . . . angle ψ of the tire 1 to be tested. The subtracting device 17 then supplies the radial force fluctuation signal **RKSk** (ψ) from which the rotational truth defect of the testing drum 4 has been removed.